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Draft Genome Sequence of Strain ATCC 33958, Reported To Be *Elizabethkingia miricola*

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We report the draft genome of *Elizabethkingia* strain ATCC 33958, which has been classified as *Elizabethkingia miricola*. Similar to other *Elizabethkingia* species, the ATCC 33958 draft genome contains numerous β-lactamase genes. ATCC 33958 also harbors a urease gene cluster which supports classification as *E. miricola*.

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The Gram-negative genus *Elizabethkingia* consists of *Elizabethkingia meningoseptica* (1–4), *Elizabethkingia anophelis* (5–7), *Elizabethkingia miricola* (3, 8), and *Elizabethkingia endophytica* (9). ATCC 33958 demonstrated 84% DNA-DNA hybridization with the *E. miricola* type strain isolated from condensation in the Russian space laboratory Mir (3, 8). Recent reports of *Elizabethkingia* draft genomes are clinically important since they support the classification of species within this genus. We now report the draft genome of ATCC 33958.

DNA was isolated from an ATCC 33958 brain heart infusion broth culture and then sequenced with a Roche 454 GS Junior. The 429,384 reads were then assembled with the Roche GS De Novo assembler (v2.7) and uploaded to the RAST server for annotation (10). The ATCC 33958 draft genome was 4,578,109 bp (75 contigs, 35.8% GC content) in length and contained 4,421 predicted coding sequences, including 46 tRNA and 3 rRNA genes.

Unlike other *Elizabethkingia* species, *E. miricola* readily hydrolyzes urea (3, 7, 8). RAST analysis revealed the presence of a urease gene cluster (*ureABCEFGD*) in ATCC 33958, which was not found in the *E. meningoseptica* (1) or *E. anophelis* (6) draft genomes.

Elizabethkingia species express a multiple antimicrobial resistance phenotype and are resistant to the action of many antimicrobials (11–13). In general, a single β-lactamase gene allows a bacterial pathogen to resist the action of β-lactams and/or related antimicrobials (14, 15). *E. meningoseptica* was the first bacterial pathogen reported to harbor three active β-lactamase genes, which encode a class D serine β-lactamase (16–18), and two unrelated metallo-β-lactamases (16, 19–22). Additionally, *Elizabethkingia* draft genomes have revealed that each species harbors numerous putative β-lactamase genes (1, 6, 23).

Putative β-lactamases identified in the ATCC 33958 RAST annotations were further analyzed with BLASTp (blast.ncbi.nlm.nih.gov) and compared to characterized β-lactamases at http://www.lahey.org/Studies/ and the BRENDA database (http://www.brenda-enzymes.org/), and β-lactamase domains were also identified by using Pfam analysis (http://pfam.sanger.ac.uk). From these analyses we surmised the presence of at least 12 putative β-lactamase genes within the ATCC 33958 draft genome located on 9 contigs. Of these putative β-lactamase genes, 4 demonstrated strong amino acid homologies (42.9% to 98.8% amino acid identity) along the entire length of 4 phenotypically characterized β-lactamases (17, 20, 24, 25). Comparison of the putative ATCC 33958 β-lactamases to one another revealed that only 2 demonstrated significant amino acid identity to each other (42%). It is known that chromosomally encoded β-lactamase genes can be induced by β-lactams and play a role in β-lactam resistance (26). The number and dissimilarity of the β-lactamases within ATCC 33958 suggest that these proteins may contribute to function(s) other than β-lactamase activity. In *Escherichia coli*, for instance, chromosomally encoded β-lactamases display penicillin-binding protein characteristics and play a role in peptidoglycan metabolism (27). The cloning of ATCC 33958 β-lactamase genes will determine if these genes do indeed encode proteins with β-lactamase activity.

Nucleotide sequence accession numbers. This whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JRFN00000000. The version described in this paper is version JRFN01000000 for ATCC 33958.

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REFERENCES

1. **Matyi SA, Hoyt PR, Hosoyama A, Yamazoe A, Fujita N, Gustafson JE.** 2013. Draft genome sequences of *Elizabethkingia meningoseptica*. Genome Announc **1**(4):e00444-13. http://dx.doi.org/10.1128/genomeA.00444-13.
2. **Brody JA, Moore H, King EO.** 1958. Meningitis caused by an unclassified Gram-negative bacterium in newborn infants. AMA J Dis Child **96:**1–5. http://dx.doi.org/10.1001/archpedi.1958.02060060003001.
3. **Kim KK, Kim MK, Lim JH, Park HY, Lee ST.** 2005. Transfer of *Chryseobacterium meningosepticum* and *Chryseobacterium miricola* to *Elizabethk-*

ingia gen. nov. as *Elizabethkingia meningoseptica* comb. nov. and *Elizabethkingia miricola* comb. nov. Int J Syst Evol Microbiol **55:**1287–1293. http://dx.doi.org/10.1099/ijs.0.63541-0.

4. **King EO**. 1959. Studies on a group of previously unclassified bacteria associated with meningitis in infants. Am J Clin Pathol **31:**241–247.
5. **Teo J, Tan SY, Liu Y, Tay M, Ding Y, Li Y, Kjelleberg S, Givskov M, Lin RT, Yang L**. 2014. Comparative genomic analysis of malaria mosquito vector-associated novel pathogen *Elizabethkingia anophelis*. Genome Biol Evol **6:**1158–1165. http://dx.doi.org/10.1093/gbe/evu094.
6. **Kukutla P, Lindberg BG, Pei D, Rayl M, Yu W, Steritz M, Faye I, Xu J**. 2013. Draft genome sequences of *Elizabethkingia anophelis* strains R26T and Ag1 from the midgut of the malaria mosquito *Anopheles gambiae*. Genome Announc **1**(6):e01030-13. http://dx.doi.org/10.1128/genomeA.01030-13.
7. **Kämpfer P, Matthews H, Glaeser SP, Martin K, Lodders N, Faye I**. 2011. *Elizabethkingia anophelis* sp. nov., isolated from the midgut of the mosquito *Anopheles gambiae*. Int J Syst Evol Microbiol **61:**2670–2675. http://dx.doi.org/10.1099/ijs.0.026393-0.
8. **Li Y, Kawamura Y, Fujiwara N, Naka T, Liu H, Huang X, Kobayashi K, Ezaki T**. 2003. *Chryseobacterium miricola* sp. nov., a novel species isolated from condensation water of space station Mir. Syst Appl Microbiol **26:**523–528. http://dx.doi.org/10.1078/072320203770865828.
9. **Kampfer P, Busse H, McInroy JA, Glaeser SP**. 9 April 2015. *Elizabethkingia endophytica* sp. nov., isolated from *Zea mays* and emended description of *Elizabethkingia anophelis* Kämpfer et al. 2011. Int J Syst Evol Microbiol http://dx.doi.org/10.1099/ijs.0.000236.
10. **Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R**. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res **42:**D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.
11. **Jean SS, Lee WS, Chen FL, Ou TY, Hsueh PR**. 2014. *Elizabethkingia meningoseptica*: an important emerging pathogen causing healthcare-associated infections. J Hosp Infect **86:**244–249. http://dx.doi.org/10.1016/j.jhin.2014.01.009.
12. **Lau SK, Wu AK, Teng JL, Tse H, Curreem SO, Tsui SK, Huang Y, Chen JH, Lee RA, Yuen KY, Woo PC**. 2015. Evidence for *Elizabethkingia anophelis* transmission from mother to infant, Hong Kong. Emerg Infect Dis **21:**232–241. http://dx.doi.org/10.3201/eid2102.140623.
13. **Lin XH, Xu YH, Sun XH, Huang Y, Li JB**. 2012. Genetic diversity analyses of antimicrobial resistance genes in clinical *Chryseobacterium meningosepticum* isolated from Hefei, China. Int J Antimicrob Agents **40:**186–188. http://dx.doi.org/10.1016/j.ijantimicag.2012.03.020.
14. **Bush K**. 2013. The ABCD's of beta-lactamase nomenclature. J Infect Chemother **19:**549–559. http://dx.doi.org/10.1007/s10156-013-0640-7.
15. **Kunz AN, Brook I**. 2010. Emerging resistant Gram-negative aerobic bacilli in hospital-acquired infections. Chemotherapy **56:**492–500. http://dx.doi.org/10.1159/000321018.
16. **Bellais S, Aubert D, Naas T, Nordmann P**. 2000. Molecular and biochemical heterogeneity of class B carbapenem-hydrolyzing beta-lactamases in *Chryseobacterium meningosepticum*. Antimicrob Agents Chemother **44:**1878–1886. http://dx.doi.org/10.1128/AAC.44.7.1878-1886.2000.
17. **Bellais S, Poirel L, Naas T, Girlich D, Nordmann P**. 2000. Genetic-biochemical analysis and distribution of the Ambler class A beta-lactamase CME-2, responsible for extended-spectrum cephalosporin resistance in *Chryseobacterium* (*Flavobacterium*) *meningosepticum*. Antimicrob Agents Chemother **44:**1–9. http://dx.doi.org/10.1128/AAC.44.1.1-9.2000.
18. **Rossolini GM, Franceschini N, Lauretti L, Caravelli B, Riccio ML, Galleni M, Frère JM, Amicosante G**. 1999. Cloning of a *Chryseobacterium* (*Flavobacterium*) *meningosepticum* chromosomal gene ($blaA_{CME}$) encoding an extended-spectrum class A beta-lactamase related to the *Bacteroides* cephalosporinases and the VEB-1 and PER beta-lactamases. Antimicrob Agents Chemother **43**(Pt 1)**:**2193–2199.
19. **Rossolini GM, Franceschini N, Riccio ML, Mercuri PS, Perilli M, Galleni M, Frere JM, Amicosante G**. 1998. Characterization and sequence of the *Chryseobacterium* (*Flavobacterium*) *meningosepticum* carbapenemase: a new molecular class B beta-lactamase showing a broad substrate profile. Biochem J **332:**145–152.
20. **Lisa MN, Hemmingsen L, Vila AJ**. 2010. Catalytic role of the metal ion in the metallo-beta-lactamase GOB. J Biol Chem **285:**4570–4577. http://dx.doi.org/10.1074/jbc.M109.063743.
21. **Morán-Barrio J, González JM, Lisa MN, Costello AL, Peraro MD, Carloni P, Bennett B, Tierney DL, Limansky AS, Viale AM, Vila AJ**. 2007. The metallo-beta-lactamase GOB is a mono-Zn(II) enzyme with a novel active site. J Biol Chem **282:**18286–18293. http://dx.doi.org/10.1074/jbc.M700467200.
22. **Vessillier S, Docquier JD, Rival S, Frere JM, Galleni M, Amicosante G, Rossolini GM, Franceschini N**. 2002. Overproduction and biochemical characterization of the *Chryseobacterium meningosepticum* BlaB metallo-beta-lactamase. Antimicrob Agents Chemother **46:**1921–1927. http://dx.doi.org/10.1128/AAC.46.6.1921-1927.2002.
23. **Quick J, Constantinidou C, Pallen MJ, Oppenheim B, Loman NJ**. 2014. Draft genome sequence of *Elizabethkingia meningoseptica* isolated from a traumatic wound. Genome Announc **2**(3)**:**e00355-14. http://dx.doi.org/10.1128/genomeA.00355-14.
24. **González LJ, Vila AJ**. 2012. Carbapenem resistance in *Elizabethkingia meningoseptica* is mediated by metallo-beta-lactamase BlaB. Antimicrob Agents Chemother **56:**1686–1692. http://dx.doi.org/10.1128/AAC.05835-11.
25. **Silva J, Aguilar C, Ayala G, Estrada MA, Garza-Ramos U, Lara-Lemus R, Ledezma L**. 2000. TLA-1: a new plasmid-mediated extended-spectrum beta-lactamase from *Escherichia coli*. Antimicrob Agents Chemother **44:**997–1003. http://dx.doi.org/10.1128/AAC.44.4.997-1003.2000.
26. **Normark S, Lindquist S, Lindberg F**. 1986. Chromosomal beta-lactam resistance in enterobacteria. Scand J Infect Dis Suppl **49:**38–45.
27. **Henderson TA, Young KD, Denome SA, Elf PK**. 1997. AmpC and AmpH, proteins related to the class C beta-lactamases, bind penicillin and contribute to the normal morphology of *Escherichia coli*. J Bacteriol **179:**6112–6121.